

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=6; day=26; hr=13; min=35; sec=45; ms=754;]

=====

Application No: 10595571 Version No: 1.0

Input Set:**Output Set:**

Started: 2009-06-17 14:42:08.813
Finished: 2009-06-17 14:42:12.850
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 37 ms
Total Warnings: 30
Total Errors: 2
No. of SeqIDs Defined: 38
Actual SeqID Count: 38

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
E 257	Invalid sequence data feature in <221> in SEQ ID (21)

Input Set:

Output Set:

Started: 2009-06-17 14:42:08.813
Finished: 2009-06-17 14:42:12.850
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 37 ms
Total Warnings: 30
Total Errors: 2
No. of SeqIDs Defined: 38
Actual SeqID Count: 38

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (24) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)

SEQUENCE LISTING

<110> FUTAMURA, MANABU
YOU, MING
ZHANG, ZHONGQIU

<120> GENE EXPRESSION AND POLYMORPHISMS ASSOCIATED WITH LUNG
CANCER

<130> 22727-04393

<140> 10595571

<141> 2009-06-17

<150> PCT/US04/35690

<151> 2004-10-27

<150> 60/514,673

<151> 2003-10-27

<160> 38

<170> PatentIn Ver. 3.3

<210> 1

<211> 716

<212> PRT

<213> Homo sapiens

<400> 1

Met	Ser	Gly	Ser	Lys	Lys	Lys	Lys	Val	Thr	Lys	Ala	Glu	Arg	Leu	Lys
1				5					10					15	

Leu	Leu	Gln	Glu	Glu	Glu	Glu	Arg	Arg	Leu	Lys	Glu	Glu	Glu	Glu	Ala
		20					25							30	

Arg	Leu	Lys	Tyr	Glu	Lys	Glu	Glu	Met	Glu	Arg	Leu	Glu	Ile	Gln	Arg
		35					40					45			

Ile	Glu	Lys	Glu	Lys	Trp	His	Arg	Leu	Glu	Ala	Lys	Asp	Leu	Glu	Arg
	50					55					60				

Arg	Asn	Glu	Glu	Leu	Glu	Glu	Leu	Tyr	Leu	Leu	Glu	Arg	Cys	Phe	Pro
65					70					75				80	

Glu	Ala	Glu	Lys	Leu	Lys	Gln	Glu	Thr	Lys	Leu	Leu	Ser	Gln	Trp	Lys
			85						90					95	

His	Tyr	Ile	Gln	Cys	Asp	Gly	Ser	Pro	Asp	Pro	Ser	Val	Ala	Gln	Glu
		100						105						110	

Met	Asn	Thr	Phe	Ile	Ser	Leu	Trp	Lys	Glu	Lys	Thr	Asn	Glu	Thr	Phe
		115					120					125			

Glu	Glu	Val	Ile	Glu	Lys	Ser	Lys	Val	Val	Leu	Asn	Leu	Ile	Glu	Lys
		130				135						140			

Leu	Lys	Phe	Ile	Leu	Leu	Glu	Thr	Pro	Pro	Cys	Asp	Leu	Gln	Asp	Lys				
145					150					155					160				
Asn	Ile	Ile	Gln	Tyr	Gln	Glu	Ser	Ile	Leu	Gln	Leu	Gln	Glu	Leu	Leu				
			165						170					175					
His	Leu	Lys	Phe	Gly	Val	Ala	Thr	Glu	Ile	Leu	Leu	Lys	Gln	Ala	Ser				
			180					185					190						
Thr	Leu	Ala	Asp	Leu	Asp	Ser	Gly	Asn	Met	Glu	Lys	Val	Ile	Lys	Asp				
		195					200					205							
Glu	Asn	Val	Thr	Leu	Tyr	Val	Trp	Ala	Asn	Leu	Lys	Lys	Asn	Pro	Arg				
	210					215					220								
His	Arg	Ser	Val	Arg	Phe	Ser	Glu	Thr	Gln	Ile	Gly	Phe	Glu	Ile	Pro				
225				230					235						240				
Arg	Ile	Leu	Ala	Thr	Ser	Asp	Ile	Ala	Val	Arg	Leu	Leu	His	Thr	His				
				245					250					255					
Tyr	Asp	His	Val	Ser	Ala	Leu	His	Pro	Val	Ser	Thr	Pro	Ser	Lys	Glu				
		260						265					270						
Tyr	Thr	Ser	Ala	Val	Thr	Glu	Leu	Val	Lys	Asp	Asp	Val	Lys	Asn	Val				
		275					280					285							
Glu	Lys	Ala	Ile	Ser	Lys	Glu	Val	Glu	Glu	Glu	Ser	Lys	Gln	Gln	Glu				
	290					295					300								
Arg	Gly	Ser	His	Leu	Ile	Gln	Glu	Glu	Glu	Ile	Lys	Val	Glu	Glu	Glu				
305				310						315						320			
Gln	Gly	Asp	Ile	Glu	Val	Lys	Met	Ser	Ser	Ala	Glu	Glu	Glu	Ser	Glu				
			325					330						335					
Ala	Ile	Lys	Cys	Glu	Arg	Glu	Met	Lys	Val	Leu	Ser	Glu	Thr	Val	Ser				
		340						345					350						
Ala	Ala	Gln	Leu	Leu	Leu	Val	Glu	Asn	Ser	Ser	Glu	Lys	Pro	Asp	Phe				
		355				360						365							
Phe	Glu	Asp	Asn	Val	Val	Asp	Leu	Cys	Gln	Phe	Thr	Thr	Leu	Gly	Gly				
	370					375				380									
Val	Tyr	His	Leu	Asp	Ile	Leu	Glu	Leu	Pro	Pro	Gln	Cys	Lys	Pro	Val				
385				390					395					400					
Lys	Gly	Trp	Met	Ile	Val	Glu	Ile	Leu	Lys	Glu	Gly	Leu	Gln	Lys	Tyr				
			405					410						415					
Thr	Tyr	Pro	Pro	Glu	Thr	Thr	Glu	Glu	Phe	Glu	Thr	Glu	Asn	Ala	Phe				
		420					425						430						
Pro	Pro	Ile	Glu	Val	Thr	Leu	Glu	Val	His	Glu	Asn	Val	Ile	Phe	Phe				
	435					440						445							

Glu Asp Pro Val Val Val Arg Trp Asp Ala Glu Gly Lys His Trp Arg
 450 455 460
 Thr Asp Gly Ile Ser Asn Val Ser Tyr Lys Pro Lys Glu Arg Leu Val
 465 470 475 480
 Thr Phe Ser Leu Asp Thr Phe Gly Pro Val Thr Leu Ile Gln Asp Ala
 485 490 495
 His Ile Asn Met Pro Tyr Gln Ser Trp Glu Leu Arg Pro Leu Asp Val
 500 505 510
 Asn Lys Val Leu Leu Thr Val Thr Thr Val Phe Thr Glu Ile Gln Ile
 515 520 525
 Gln Ile Lys Glu Asn Leu Cys Met Leu Ser Ser Ile Lys Leu Lys Asp
 530 535 540
 Lys Lys His Ile Ser Ile Leu Glu Gly Thr Trp Met Thr Pro Ile Pro
 545 550 555 560
 Phe Ile Ile Ala Leu Lys Glu Ala Gly Leu Asn Ile Phe Pro Thr Arg
 565 570 575
 His Ser His Phe Tyr Val Ile Ile Asn Asn Lys Val Pro Leu Val Glu
 580 585 590
 Val Lys Ala Tyr Arg Gln Met Ala Leu Leu Ser Ser Ala Phe Ala Phe
 595 600 605
 Gly Trp Ser Lys Trp Asn Leu Leu Cys Asn Ser Thr Lys Val Val Phe
 610 615 620
 Lys Val Arg Glu His Leu Thr Glu Glu Cys Thr Glu Asn Pro Asn Trp
 625 630 635 640
 Ala Leu Leu Met Phe Ser Gly Asp Arg Ala Gln Arg Leu Lys Ile Lys
 645 650 655
 Glu Glu Ser Glu Ala Phe Ser Glu Ala Leu Lys Glu Glu Thr Glu Phe
 660 665 670
 His Ser Thr Leu Tyr His Met Val Lys Asp Phe Ala Ser Glu Glu Ala
 675 680 685
 Met Glu Lys Val Arg Ser Ser Asn Cys Gln Phe Val Asn Ser Val Cys
 690 695 700
 His Met Leu Leu Ser Thr Arg Leu Leu Ser Tyr Ser
 705 710 715

<210> 2

<211> 2151

<212> DNA

<213> Homo sapiens

<400> 2

```
atgtctggca gtaagaaaaa gaaagtcacc aaagctgaac gattgaagct gctacaagag 60
gaggaggaga gacgactgaa agaggaagag gaagcccgtt tgaaatatga gaaagaagaa 120
atggaaaggc ttgaaataca gcgaattgag aaagaaaaat ggcatcgact tgaagcaaaa 180
gatctagaaa ggagaaatga agaacttgaa gaactttatt tattagagag gtgttttcct 240
gaagcagaga aattgaaaca ggaaactaaa ttgctttctc agtggaaagca ctacattcaa 300
tgtgatggga gtcctgatcc ttcagtagcc caagaaatga acacgtttat tagtttgtgg 360
aaagagaaaa caaatgagac ttttgaggaa gtgattgaga agagtaaagt agtgctaaat 420
ttaattgaga aattgaaatt ttttttactg gaaactccac catgtgattt gcaagataaa 480
aatataatag agtaccaaga atcaatacta caactgcagg agctccttca tcttaaattc 540
ggtgtagcca cagaaatact tctcaaacaa gctagtactt tggcagatct ggacagtgga 600
aatatggaaa aagtcattaa agatgaaaat gttactctgt atgtgtgggc aaacctcaag 660
aagaatccaa ggcacagaag tgtagattc tctgaaacac aaattggatt tgagattcca 720
aggatattag caacaagtga cattgctgta cgactcctgc ataccacta tgatcatgtt 780
tctgcactgc accctgtttc aacaccatca aaagaatata cttctgcagt aactgagctt 840
gtcaaagatg atgttaagaa tgtagaaaaa gcaatcagca aggaggtcga agaagagtcc 900
aaacaacaag aaagagggtc tcacttaatt caggaggaag aaataaaagt tgaggaggaa 960
caaggtgata ttgaagtga aatgagttct gctgaggaag aatctgaagc cataaaatgt 1020
gaacgagaga tgaaagtatt aagtgaact gtttcagcag cacagttgtt gctggtagag 1080
aattcttctg aaaagccaga tttctttgaa gacaatgtgg tggatttatg ccagttcaca 1140
actctgggtg gagtatacca cttggatatt ttggagcttc ctccacagtg taaaccagtg 1200
aagggatgga tgattgtgga aatactcaaa gaaggattac agaaatacac atatcctccg 1260
gaaactacag aagagtttga gacagaaaat gctttccac ctatagaggt cacacttgag 1320
gttcattgaga atgtaatctt ttttgaggat cctgtggttg taaggtggga tgctgaaggt 1380
aaacattgga gaactgatgg catcagcaat gtatcctaca aacaaaaga aagacttgta 1440
acattcagcc tggacacctt tggccctgtt accttgattc aagatgctca tattaacatg 1500
ccgtaccagt catgggaact aagaccactt gatgtaaata aagtactttt aactgtgact 1560
acagtattta ctgagattca aatacaaat aaggaaaacc tctgcatgtt atcttcaatc 1620
aaactaaaag acaagaaaca catctctatt ttggaaggaa cctggatgac tcctattcct 1680
ttcattattg ctttgaaaga agctggactg aatatctttc ctactagaca ctctcatttt 1740
tatgttatta taaacaataa ggttcctttg gtagaagtga aagcttatcg acagatggcc 1800
ctactaagtt ctgcttttgc atttgggttg agcaagtgga acctactatg taattctaca 1860
aaagtcgtat ttaaggtgag ggaacacctt actgaagaat gtactgagaa tcctaattgg 1920
gcccttttaa tgtttagtgg tgacagagca caaagactga agatcaagga agagagtgag 1980
gcattttctg aagcacttaa agaagaaact gagtttcatt ctactttata tcacatgggtg 2040
aaggattttg cttctgagga agcaatggag aaagtcagga gttccaactg tcagtttgtc 2100
aactctgtgt gccacatgct gctctctacc agattgctca gctactccta a 2151
```

<210> 3

<211> 730

<212> PRT

<213> Mus sp.

<400> 3

```
Met Ala Pro Lys Ser Lys Lys Ala Pro Ser Lys Lys Lys Met Thr Lys
  1                      5                      10                     15

Ala Glu Arg Leu Arg Leu Met Gln Glu Glu Glu Arg Arg Leu Lys
      20                      25                     30

Glu Glu Glu Glu Ala Arg Leu Lys Phe Glu Lys Glu Glu Gln Glu Arg
      35                      40                     45

Leu Glu Ile Gln Arg Ile Glu Arg Glu Lys Trp Asn Leu Leu Glu Lys
      50                      55                     60
```

Lys Asp Leu Glu Arg Arg Ser Gln Glu Leu Glu Glu Leu Ala Leu Leu
 65 70 75 80

Glu Gly Cys Phe Pro Glu Ala Glu Lys Gln Lys Arg Glu Ile Arg Ala
 85 90 95

Leu Ala Gln Trp Lys His Tyr Thr Glu Cys Asp Gly Ser Pro Asp Pro
 100 105 110

Trp Val Ala Gln Glu Met Asn Thr Phe Ile Ser Leu Trp Glu Glu Glu
 115 120 125

Lys Asn Gln Ala Phe Glu Gln Val Met Glu Lys Ser Lys Leu Val Leu
 130 135 140

Ser Leu Ile Glu Lys Val Lys Leu Ile Leu Leu Glu Thr Pro Thr Tyr
 145 150 155 160

Glu Leu Asp His Arg Thr Val Leu Gln His Gln Gly Ser Ile Leu Arg
 165 170 175

Leu Gln Glu Leu Leu Ser Leu Lys Ile Asn Val Ala Thr Glu Leu Leu
 180 185 190

Leu Arg Gln Ala Ser Asn Leu Ala Asp Leu Asp Thr Gly Asn Met Glu
 195 200 205

Lys Ile Ile Lys Asp Glu Asn Val Thr Leu Tyr Val Trp Ala Asn Leu
 210 215 220

Lys Lys Asn Pro Arg His Arg Ser Val Arg Phe Ser Glu Thr Gln Ile
 225 230 235 240

Gly Phe Glu Ile Pro Arg Ile Leu Ala Thr Ser Asn Val Ala Leu Arg
 245 250 255

Leu Leu His Thr Arg Tyr Asp His Ile Thr Pro Leu Phe Pro Ile Ala
 260 265 270

Val Thr Glu Gln Asn Gln Asn Pro Val Gly Ala Glu Gln Val Asn Val
 275 280 285

Glu Glu Ser Thr Glu Lys Ala Met Thr Glu Glu Lys Leu Phe Thr Glu
 290 295 300

Glu Lys Ala Ala Asn Glu Asp Glu Gln Pro Lys Ala Glu Gln Glu Arg
 305 310 315 320

Glu Leu Asn Leu Val Gln Glu Glu Asn Lys Tyr Glu Ala Ile Glu Asn
 325 330 335

Thr Val Leu Gln Arg Thr Ser Asp Ser Glu Gly Glu Asp Ser Gln Thr
 340 345 350

Thr Gln Leu Glu Leu Glu Met Lys Leu Leu Ser Glu Ala Val Leu Ala
 355 360 365

Ala	Gln	Leu	Cys	Leu	Val	Glu	Asn	Val	Val	Glu	Leu	Pro	Glu	Ala	Ser		
370						375						380					
Gln	Ala	Tyr	Lys	Val	Asp	Leu	Cys	His	Phe	Ser	Thr	Leu	Gly	Gly	Val		
385					390					395					400		
Tyr	His	Leu	Asp	Val	Leu	Glu	Leu	Pro	Pro	Gln	Cys	Lys	Pro	Val	Lys		
				405					410					415			
Gly	Trp	Val	Leu	Val	Glu	Ile	Leu	Gln	Glu	Gly	Leu	Gln	Arg	Phe	Ile		
			420					425					430				
Tyr	Pro	Pro	Asp	Thr	Thr	Glu	Glu	Pro	Asp	Pro	Asp	Val	Thr	Phe	Pro		
	435							440				445					
Pro	Ile	Glu	Val	Thr	Leu	Glu	Ile	His	Lys	Ser	Val	Ile	Phe	Phe	Glu		
450						455					460						
Arg	Pro	Arg	Val	Val	Arg	Trp	Asp	Asn	Glu	Gly	Lys	Phe	Trp	Arg	Ser		
465					470					475					480		
Asp	Gly	Ile	Ser	Ser	Val	Tyr	Tyr	Asn	Arg	Glu	Asp	Arg	Leu	Leu	Thr		
				485					490					495			
Phe	Ser	Met	Asp	Thr	Leu	Gly	Pro	Val	Thr	Leu	Ile	Gln	Asp	Ala	His		
		500						505					510				
Val	Asn	Met	Pro	Tyr	Gln	Ser	Trp	Glu	Met	Ser	Pro	Cys	Gly	Met	Asn		
	515						520					525					
Lys	Val	Leu	Leu	Ile	Val	Lys	Thr	Val	Phe	Met	Glu	Leu	Gln	Ile	Tyr		
530						535					540						
Ile	Lys	Glu	Asn	Leu	Cys	Met	Leu	Ala	Ser	Val	Lys	Leu	Arg	Gly	Lys		
545					550					555					560		
Gly	Leu	Glu	Phe	His	Leu	Lys	Gly	Lys	Trp	Met	Ala	Pro	Ile	Pro	Phe		
				565					570					575			
Ile	Leu	Ala	Leu	Lys	Glu	Ala	Gly	Leu	Asn	Ile	Phe	Pro	Ala	Val	Tyr		
		580						585					590				
Ser	His	Phe	Tyr	Val	Val	Ile	Asn	Asn	Lys	Val	Pro	Gln	Val	Glu	Leu		
	595						600					605					
Lys	Ala	Tyr	Arg	Gln	Met	Ala	Leu	Leu	Ser	Ser	Ala	Phe	Ser	Phe	Gly		
610					615						620						
Trp	Ser	Lys	Trp	Asn	Met	Val	Cys	Asn	Ser	Thr	Arg	Val	Val	Ile	Arg		
625					630					635					640		
Val	Arg	Glu	Gln	Leu	Ser	Glu	Glu	Thr	Glu	His	His	Thr	Trp	Ser	Leu		
				645					650					655			
Leu	Met	Phe	Ser	Gly	Asp	Arg	Ala	Gln	Met	Leu	Lys	Met	Gln	Glu	Glu		
	660							665					670				

Asn Asp Lys Phe Ser Glu Ala Leu Arg Glu Gly Thr Glu Phe His Ser
675 680 685

Thr Leu Tyr His Met Met Lys Asp Phe Ala Ser Pro Val Ala Met Glu
690 695 700

Arg Val Arg His Ser Asn Cys Gln Phe Ile Asp Ser Val Cys Tyr Met
705 710 715 720

Leu Leu Ser Ile Arg Val Leu Ser Tyr Ser
725 730

<210> 4

<211> 2413

<212> DNA

<213> Mus sp.

<400> 4

ttgtgagtg gcggtggcctg tcgtcttgac aaccgtgagc gttcctgctc tgcagcgttc 60
acttttcctt aagcaaagt cctgcttctg tcatggctcc caaatcaaaa aaggctcca 120
gtaagaaaaa gatgaccaa gccgagcgac tgcggtgat gcaggaggag gaggagagac 180
gcctgaagga ggaagaagag gcgcggctga aatttgaaaa agaagaacag gaaaggctag 240
aaatacagcg gattgagaga gagaagtgga atctgctgga aaagaaagac ctagaacgaa 300
gaagccaaga gcttgaagag cttgctctgc tcgagggttg ttttcctgaa gcagagaaac 360
agaagcggga aattcgagct ctggtctcagt ggaagcacta cacggagtgt gatgggagcc 420
ccgacccttg ggttgcccag gaaatgaaca cgttcattag cctgtgggaa gaggagaaga 480
accaggcctt tgaacaagt atggagaaaa gcaaactggg gctgtcgttg attgaaaagg 540
tgaagttaat ttactggaa actccgacat atgagctgga ccacaggact gtcctgcagc 600
atcaagggtc aattctgcgc ctacaagagc tgctcagcct gaagatcaac gtggccacag 660
aactacttct tcgacaagct agtaacttag cagatctgga cactgggaat atggagaaaa 720
tcatcaaaaga tgagaatgtc accctgtacg tgtgggcaaa cctcaaaaag aatccaaggc 780
accggagtgt gaggttctca gagacacaaa ttggatttga aatccaagg atcctggcca 840
cgagcaatgt tgctcttcgg cttctacaca cacgctatga ccacatcaca cccttgttcc 900
ccattgccgt cactgagcaa aatcaaaacc ccgtgggagc agagcaagtc aacgtcgagg 960
aaagtacaga aaaggccatg actgaagaaa agctctttac tgaagaaaaa gctgccaacg 1020
aagatgagca gccaaggct gaacaggaaa gagagctcaa cttggttcaa gaggagaaca 1080
aatatgaagc tatagagaac actgtcttac aaaggacttc cgactctgaa ggggaggatt 1140
cccaaaccac ccaacttgaa ctggagatga agctgctgag tgaagcagtc ttagcagcac 1200
agctgtgcct ggtagagaat gtggtggaat tgccagaagc ctcaacaagc tacaagggtg 1260
acttgtgcca tttctctacc ctgggcgggc tgtaccacct ggatgttctg gagctgcccc 1320
ctcagtgtcaa gcctgtgaag ggctgggtgc tagtggagat actccaggaa ggactgcaga 1380
ggtttatata tcctccagac accacagagg aacctgatcc agacgtcacc ttcccacca 1440
tagaggtcac actggagatc cacaagagcg tcatcttctt tgagcgccct agggctcgtc 1500
ggtgggacaa tgaaggtaaa ttctggcggg cagatggcat cagcagtgtc tattacaacc 1560
gagaagacag gctcctaacc ttcagtatgg atactttggg ccctgtgacc ttgattcagg 1620
atgctcacgt gaacatgcct taccagtcct gggagatgag tcctgtggc atgaacaaag 1680
tccttcta at agtgaagacg gttttcatgg agctccagat atacatcaag gaaaacctct 1740
gcatgctggc ttcagtga aa ctgaggggca agggactcga gtttcatcta aaaggaaaat 1800
ggatggctcc tatacccttc attctggctt tgaaagaggc cgggctgaac atcttcctctg 1860
ctgtatactc ccatttttat gtggtcatca acaataagg accc